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1632

1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658C

DATE: 08/06/2002

TIME: 17:02:16

Input Set : A:\55924.app

Output Set: N:\CRF3\08062002\I729658C.raw

P.6

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3 <110> APPLICANT: Zonana et al.
5 <120> TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
7 <130> FILE REFERENCE: 55924
9 <140> CURRENT APPLICATION NUMBER: 09/729,658C
10 <141> CURRENT FILING DATE: 2000-12-04
12 <150> PRIOR APPLICATION NUMBER: 09/342,681
13 <151> PRIOR FILING DATE: 1999-06-29
15 <150> PRIOR APPLICATION NUMBER: 60/092,279
16 <151> PRIOR FILING DATE: 1998-07-09
18 <150> PRIOR APPLICATION NUMBER: 60/112,366
19 <151> PRIOR FILING DATE: 1998-12-15
21 <160> NUMBER OF SEQ ID NOS: 127
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1574
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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31 <221> NAME/KEY: CDS
32 <222> LOCATION: (242)..(1417)
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39 ggaacgggtc cctgcagccc ccagccgatg gcaggacagt agccgctgt cagaggtcgt 180
41 gaacggctga ggcagacgca gggctcccg ggcctcaaga gagtgggtgt ctccggaggc 240
43 c atg ggc tac ccg gag gtg gag cgc agg gaa ctc ctg cct gca gca gcg 289
44 Met Gly Tyr Pro Glu Val Glu Arg Arg Glu Leu Leu Pro Ala Ala Ala
45 1 5 10 15
47 ccg cgg gag cga ggg agc cag ggc tgc ggg tgt ggc ggg gcc cct gcc 337
48 Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
49 20 25 30
51 cgg gcg ggc gaa ggg aac agc tgc ctg ctc ttc ctg ggt ttc ttt ggc 385
52 Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
53 35 40 45
55 ctc tcg ctg gcc ctc cac ctg ctg acg ttg tgc tgc tac cta gag ttg 433
56 Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
57 50 55 60
59 cgc tcg gag ttg cgg cgg gaa cgt gga gcc gag tcc cgc ctt ggc ggc 481
60 Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
61 65 70 75 80
63 tcg ggc acc cct ggc acc tct ggc acc cta agc agc ctc ggt ggc ctc 529
64 Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
65 85 90 95

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67 gac cct gac agc ccc atc acc agt cac ctt ggg cag ccg tca cct aag 577
68 Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
69 100 105 110
71 cag cag cca ttg gaa ccg gga gaa gcc gca ctc cac tct gac tcc cag 625
72 Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
73 115 120 125
75 gac ggg cac cag atg gcc cta ttg aat ttc ttc ttc cct gat gaa aag 673
76 Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
77 130 135 140
79 cca tac tct gaa gaa gaa agt agg cgt gtt cgc cgc aat aaa aga agc 721
80 Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
81 145 150 155 160
83 aaa agc aat gaa gga gca gat ggc cca gtt aaa aac aag aaa aag gga 769
84 Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
85 165 170 175
87 aag aaa gca gga cct cct gga ccc aat ggc cct cca gga ccc cca gga 817
88 Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
89 180 185 190
91 cct cca gga ccc cag gga ccc cca gga att cca ggg att cct gga att 865
92 Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
93 195 200 205
95 cca gga aca act gtt atg gga cca cct ggt cct cca ggt cct cct ggt 913
96 Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
97 210 215 220
99 cct caa gga ccc cct ggc ctc cag gga cct tct ggt gct gct gat aaa 961
100 Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
101 225 230 235 240
103 gct gga act cga gaa aac cag cca gct gtg gtg cat cta cag ggc caa 1009
104 Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
105 245 250 255
107 ggg tca gca att caa gtc aag aat gat ctt tca ggt gga gtg ctc aat 1057
108 Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn
109 260 265 270
111 gac tgg tct cgc atc act atg aac ccc aag gtg ttt aag cta cat ccc 1105
112 Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
113 275 280 285
115 cgc agc ggg gag ctg gag gta ctg gtg gac ggc acc tac ttc atc tat 1153
116 Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
117 290 295 300
119 agt cag gta gaa gta tac tac atc aac ttc act gac ttt gcc agc tat 1201
120 Ser Gln Val Glu Val Tyr Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
121 305 310 315 320
123 gag gtg gtg gtg gat gag aag ccc ttc ctg cag tgc aca cgc agc atc 1249
124 Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
125 325 330 335
127 gag acg ggc aag acc aac tac aac act tgc tat acc gca ggc gtc tgc 1297
128 Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
129 340 345 350
131 ctc ctc aag gcc cgg cag aag atc gcc gtc aag atg gtg cac gct gac 1345

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132 Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
133          355          360          365
135 atc tcc atc aac atg agc aag cac acc acg ttc ttt ggg gcc atc agg 1393
136 Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
137          370          375          380
139 ctg ggt gaa gcc cct gca tcc tag attcccccat tttgcctctg tccgtgcccc 1447
140 Leu Gly Glu Ala Pro Ala Ser
141 385          390
143 ttccctgggt ttgggagcca ggactcccaa aacctctaag tgctgctgtg gagtgaggtg 1507
145 tattggtgtt gcagccgcag agaaatgccc cattgttatt tattccccag tgactccagg 1567
147 gtgacaa
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151 <211> LENGTH: 391
152 <212> TYPE: PRT
153 <213> ORGANISM: Homo sapiens
155 <400> SEQUENCE: 2
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157 1          5          10          15
158 Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly Cys Gly Gly Ala Pro Ala
159          20          25          30
160 Arg Ala Gly Glu Gly Asn Ser Cys Leu Leu Phe Leu Gly Phe Phe Gly
161          35          40          45
162 Leu Ser Leu Ala Leu His Leu Leu Thr Leu Cys Cys Tyr Leu Glu Leu
163          50          55          60
164 Arg Ser Glu Leu Arg Arg Glu Arg Gly Ala Glu Ser Arg Leu Gly Gly
165          65          70          75          80
166 Ser Gly Thr Pro Gly Thr Ser Gly Thr Leu Ser Ser Leu Gly Gly Leu
167          85          90          95
168 Asp Pro Asp Ser Pro Ile Thr Ser His Leu Gly Gln Pro Ser Pro Lys
169          100          105          110
170 Gln Gln Pro Leu Glu Pro Gly Glu Ala Ala Leu His Ser Asp Ser Gln
171          115          120          125
172 Asp Gly His Gln Met Ala Leu Leu Asn Phe Phe Phe Pro Asp Glu Lys
173          130          135          140
174 Pro Tyr Ser Glu Glu Glu Ser Arg Arg Val Arg Arg Asn Lys Arg Ser
175          145          150          155          160
176 Lys Ser Asn Glu Gly Ala Asp Gly Pro Val Lys Asn Lys Lys Lys Gly
177          165          170          175
178 Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly Pro Pro Gly Pro Pro Gly
179          180          185          190
180 Pro Pro Gly Pro Gln Gly Pro Pro Gly Ile Pro Gly Ile Pro Gly Ile
181          195          200          205
182 Pro Gly Thr Thr Val Met Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
183          210          215          220
184 Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro Ser Gly Ala Ala Asp Lys
185          225          230          235          240
186 Ala Gly Thr Arg Glu Asn Gln Pro Ala Val Val His Leu Gln Gly Gln
187          245          250          255
188 Gly Ser Ala Ile Gln Val Lys Asn Asp Leu Ser Gly Gly Val Leu Asn

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189          260          265          270
190 Asp Trp Ser Arg Ile Thr Met Asn Pro Lys Val Phe Lys Leu His Pro
191          275          280          285
192 Arg Ser Gly Glu Leu Glu Val Leu Val Asp Gly Thr Tyr Phe Ile Tyr
193          290          295          300
194 Ser Gln Val Glu Val Tyr Ile Asn Phe Thr Asp Phe Ala Ser Tyr
195 305          310          315          320
196 Glu Val Val Val Asp Glu Lys Pro Phe Leu Gln Cys Thr Arg Ser Ile
197          325          330          335
198 Glu Thr Gly Lys Thr Asn Tyr Asn Thr Cys Tyr Thr Ala Gly Val Cys
199          340          345          350
200 Leu Leu Lys Ala Arg Gln Lys Ile Ala Val Lys Met Val His Ala Asp
201          355          360          365
202 Ile Ser Ile Asn Met Ser Lys His Thr Thr Phe Phe Gly Ala Ile Arg
203          370          375          380
204 Leu Gly Glu Ala Pro Ala Ser
205 385          390
209 <210> SEQ ID NO: 3
210 <211> LENGTH: 1661
211 <212> TYPE: DNA
212 <213> ORGANISM: Mus musculus
214 <220> FEATURE:
215 <221> NAME/KEY: CDS
216 <222> LOCATION: (142)..(1275)
218 <400> SEQUENCE: 3
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221 cgtgaaggac tgaggcagag gcagaggctc ccggagaggc agaggctccc gggcctcaga 120
223 tagtggttgt ctctggaggc c atg ggc tac cca gag gta gag cgc agg gaa 171
224          Met Gly Tyr Pro Glu Val Glu Arg Arg Glu
225          1          5          10
227 ccc ctg cct gcg gca gcg cca agg gag cgg ggc agc cag ggc tgc ggc 219
228 Pro Leu Pro Ala Ala Ala Pro Arg Glu Arg Gly Ser Gln Gly Cys Gly
229          15          20          25
231 tgt cgc ggg gcc cct gct cgg gcg ggc gaa ggg aac agc tgc cgg ctc 267
232 Cys Arg Gly Ala Pro Ala Arg Ala Gly Glu Gly Asn Ser Cys Arg Leu
233          30          35          40
235 ttc ctg ggt ttc ttt ggc ctc tcg ctg gcc ctc cac ctg ctg acg ctg 315
236 Phe Leu Gly Phe Phe Gly Leu Ser Leu Ala Leu His Leu Leu Thr Leu
237          45          50          55
239 tgc tgc tac cta gag ttg cgg tcc gaa ttg cgg cgg gaa cgg gga acc 363
240 Cys Cys Tyr Leu Glu Leu Arg Ser Glu Leu Arg Arg Glu Arg Gly Thr
241          60          65          70
243 gag tcc cgc ctc ggt ggc ccg ggt gct cct ggc acc tct ggc acc cta 411
244 Glu Ser Arg Leu Gly Gly Pro Gly Ala Pro Gly Thr Ser Gly Thr Leu
245 75          80          85          90
247 agc agc cct ggg agc ctc gac ccg gtg ggt ccc atc acc cgc cac ctg 459
248 Ser Ser Pro Gly Ser Leu Asp Pro Val Gly Pro Ile Thr Arg His Leu
249          95          100          105
251 ggg cag ccg tcc ttt caa cag cag cct ttg gaa ccg gga gaa gat cca 507

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252 Gly Gln Pro Ser Phe Gln Gln Gln Pro Leu Glu Pro Gly Glu Asp Pro
253      110      115      120
255 ctc ccc cct gag tcc cag gac cgg cac cag atg gcc ctc ctg aat ttc 555
256 Leu Pro Pro Glu Ser Gln Asp Arg His Gln Met Ala Leu Leu Asn Phe
257      125      130      135
259 ttc ttt cct gat gaa aag gca tat tct gaa gag gaa agt agg cgt gtt 603
260 Phe Phe Pro Asp Glu Lys Ala Tyr Ser Glu Glu Glu Ser Arg Arg Val
261      140      145      150
263 cgc cgc aat aag aga agc aaa agt ggt gaa gga gca gat ggt cct gtt 651
264 Arg Arg Asn Lys Arg Ser Lys Ser Gly Glu Gly Ala Asp Gly Pro Val
265 155      160      165      170
267 aaa aac aag aaa aag gga aag aag gca ggg cca cct ggg ccc aac ggc 699
268 Lys Asn Lys Lys Lys Gly Lys Lys Ala Gly Pro Pro Gly Pro Asn Gly
269      175      180      185
271 ccc cca gga cct cca gga cct ccg gga ccc cag gga cct cca ggg att 747
272 Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Gln Gly Pro Gly Ile
273      190      195      200
275 cca gga att cct ggg att cca gga aca act gtt atg gga cca cct ggc 795
276 Pro Gly Ile Pro Gly Ile Pro Gly Thr Thr Val Met Gly Pro Pro Gly
277      205      210      215
279 cca cct ggc cct cct ggt cct caa gga ccc cct ggc ctc caa gga cct 843
280 Pro Pro Gly Pro Pro Gly Pro Gln Gly Pro Pro Gly Leu Gln Gly Pro
281      220      225      230
283 tct ggt gct gct gat aaa act gga act cgg gaa aat cag cca gct gtg 891
284 Ser Gly Ala Ala Asp Lys Thr Gly Thr Arg Glu Asn Gln Pro Ala Val
285 235      240      245      250
287 gtg cat ctg cag ggc caa ggg tca gca att caa gtc aaa aat gat ctt 939
288 Val His Leu Gln Gly Gln Gly Ser Ala Ile Gln Val Lys Asn Asp Leu
289      255      260      265
291 tca ggt gga gtg ctc aat gac tgg tct cgc atc act atg aac cct aag 987
292 Ser Gly Gly Val Leu Asn Asp Trp Ser Arg Ile Thr Met Asn Pro Lys
293      270      275      280
295 gtg ttt aaa cta cat ccc cgc agc ggg gag ctg gag gtc tac tac atc 1035
296 Val Phe Lys Leu His Pro Arg Ser Gly Glu Leu Glu Val Tyr Tyr Ile
297      285      290      295
299 aac ttc act gac ttt gcc agc tac gag gtg gtg gtg gat gag aag ccc 1083
300 Asn Phe Thr Asp Phe Ala Ser Tyr Glu Val Val Val Asp Glu Lys Pro
301      300      305      310
303 ttc ctg cag tgc acc cgc agc att gag aca ggg aag acc aac tac aac 1131
304 Phe Leu Gln Cys Thr Arg Ser Ile Glu Thr Gly Lys Thr Asn Tyr Asn
305 315      320      325      330
307 act tgc tat act gca ggc gtg tgc ctc ctc aag gcc agg cag aaa atc 1179
308 Thr Cys Tyr Thr Ala Gly Val Cys Leu Leu Lys Ala Arg Gln Lys Ile
309      335      340      345
311 gcc gtg aag atg gtg cac gct gac atc tct atc aat atg agc aag cac 1227
312 Ala Val Lys Met Val His Ala Asp Ile Ser Ile Asn Met Ser Lys His
313      350      355      360
315 acc acc ttc ttc ggg gcc atc agg ctg ggc gaa gcc cct gca tcc tag 1275
316 Thr Thr Phe Phe Gly Ala Ile Arg Leu Gly Glu Ala Pro Ala Ser

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 65
Seq#:9; N Pos. 754
Seq#:11; N Pos. 302
Seq#:12; N Pos. 2961,3423,3673
Seq#:43; N Pos. 39
Seq#:95; N Pos. 133,168,212,239,280,427,428,429
Seq#:97; N Pos. 453,533,579
Seq#:101; N Pos. 330,331,337,357,368,379,380,383,394,395,398,401,417,419
Seq#:101; N Pos. 423,434,435,436,442,443,447,448,450,452,454,457,460,462
Seq#:101; N Pos. 463,467,469,470,485,486,489,492,494,499,504,508,509,511
Seq#:101; N Pos. 518,522,534,537,542,544,545,559,572,574,586,597,602,603
Seq#:101; N Pos. 607,615,623,627,629,631,638,641,642,651,664,665,668,669
Seq#:101; N Pos. 673,690,695,697,706,717,718,719,731,742,743,753,757,760
Seq#:101; N Pos. 767,806,815,832,839,871,1163
Seq#:103; N Pos. 300,307
Seq#:105; N Pos. 325,397,400,403,416,433,441,454,460,462,474,479,487,495
Seq#:105; N Pos. 497,499,519,549,555,574,642
Seq#:109; N Pos. 190
Seq#:111; N Pos. 64,473,489,583,604,613,625,627,632,637,640,679,699,717,752
Seq#:112; N Pos. 19
Seq#:113; N Pos. 210,213,219,222,225
Seq#:115; N Pos. 8,9,16,26,37,41,54,60,61,62,83,88,92,95,98,100,102,105,109
Seq#:115; N Pos. 114,117,123,131,139,141,144,148,154,155,157,165,171,177
Seq#:115; N Pos. 185,187,188,189,193,202,204
Seq#:116; N Pos. 528,626,665,2141,2665,2721,2722,2756